IN THE CLAIMS:

Claim 1 (Currently Amended) A method for identifying a medical condition status of a host suspected of having the medical condition ~~an object of interest as belonging to a latent class~~, the method comprising the steps of:

identifying at least one gene ~~object~~ of interest related to the medical condition;

~~(a)~~ providing at least one observation ~~related to~~ on the gene ~~object~~;

~~(b)~~ assigning the at least one observation on the gene to form a first dimension ~~as~~ of a matrix in a multidimensional space~~, said matrix having at least two directions for each gene object of interest in said space~~;

acquiring at least one sample of interest from the host;

providing at least one observation on the sample;

assigning the at least one observation on the sample to the matrix to form a second dimension;

~~(c)~~ identifying at least one latent class of each gene in a first dimension ~~object;~~ ~~and~~

identifying at least one latent class of each sample in a second dimension;

~~(d)~~ calculating the likelihood that the at least one gene ~~object~~ of interest belongs to the at least one identified latent class for the first dimension~~.~~;

calculating the likelihood that the at least one sample of interest belongs to the at least one identified latent class for the second dimension;

identifying the gene as being linked to the medical condition based upon the likelihood calculations; and

identifying the medical condition status in a host suspected of having the medical condition.

Claim 2 (Currently Amended) The method of claim 1 wherein the step of identifying at least one latent class of each gene of interest ~~object~~ further comprises, identifying at least one latent class of each gene of interest ~~object~~ according to a formula:

$$f(\bar{Y}_{j_1,\ldots,\ j_K}) \mid \left\{ j_k \in S_{km_{jk}} \right\}_{k=1}^{K} \sim G\left[ h\left( k, j_k, \left\{ \left\{ S_{km} \right\}_{m=1}^{M_k} \right\}_{k=1}^{K} \right) \right]$$

wherein $k \in \{1,\ldots K\}$ indexes the directions of the multidimensional space; $j_k \in \{1,\ldots N_k\}$ identifies an object in direction k; $N_k$ is the number of objects in principal direction k; $\vec{Y}_{j_1,\ldots,j_k}$ is a vector of one or more observations on a set of objects $\{j_1,\ldots,j_k\}$; $m \in \{1,\ldots,M_k\}$ indexes latent classes in direction k with $M_k$ being the number of latent classes in direction k; $S_{km}$ is a latent class m in direction k; $G(\cdot)$ is a specified univariate or multivariate distribution; and $f(\cdot)$ and $g(\cdot)$ are specified functions.

Claim 3 (Currently Amended) ~~The method of claim 1 wherein said objects are classified sequentially.~~

The method of claim 1 wherein the step of identifying at least one latent class of each sample of interest further comprises, identifying at least one latent class of each sample of interest according to a formula:

$$f(\vec{Y}_{j_1,\ldots,j_K}) \mid \left\{j_k \in S_{km_{jk}}\right\}_{k=1}^{K} \sim G\left[h\left(k, j_k, \left\{\left\{S_{km}\right\}_{m=1}^{M_k}\right\}_{k=1}^{K}\right)\right]$$

wherein $k \in \{1,\ldots K\}$ indexes the directions of the multidimensional space; $j_k \in \{1,\ldots N_k\}$ identifies an object in direction k; $N_k$ is the number of objects in principal direction k; $\vec{Y}_{j_1,\ldots,j_k}$ is a vector of one or more observations on a set of objects $\{j_1,\ldots,j_k\}$; $m \in \{1,\ldots,M_k\}$ indexes latent classes in direction k with $M_k$ being the number of latent classes in direction k; $S_{km}$ is a latent class m in direction k; $G(\cdot)$ is a specified univariate or multivariate distribution; and $f(\cdot)$ and $g(\cdot)$ are specified functions.

Claim 4 (Currently Amended) A method for identifying at least one gene linked to a cellular phenotype comprising:

(a) recording in a matrix one or more measurements on each of the genes subjected to a series of experimental or observational conditions, said measurements forming a first direction in a multidimensional space;

(b) providing measurements on a cell or tissue samples subjected to the essentially same series of experimental or observational conditions as in step (a), said measurements forming a second direction;

(c) identifying latent classes of the genes in the first direction, and latent classes of cell or tissue samples in the second direction~~, according to formula:~~

(d) calculating the likelihood that each gene is a member of each identified latent class for the first direction, while also calculating, simultaneously or serially, the likelihood that each cell or tissue sample is a member of each identified latent class for the second direction~~.~~; and

(e) identifying a gene as linked to a cellular phenotype based upon the likelihood that the gene is a member of each identified latent class for the first direction and upon the likelihood that each cell or tissue sample is a member of each identified latent class for the second direction.

Claim 5 (Previously Amended) The method according to claim 4 wherein the step of identifying latent classes of the genes in the first direction, and latent classes of cell or tissue samples in the second direction further comprises, identifying according to formula:

$$\log(Y_{ij}) \mid i \in S_m, j \in G_l \sim N\left[t_{il} + f(\alpha_{mi}, \beta_{lj}, \gamma_{ml}), \sigma^2\right],$$

wherein $N[.]$ refers to a Gaussian distribution; $S_m$ is a latent class m in the first direction; $G_l$ is a latent class 1 in the second direction; and $f(\alpha_{mi}, \beta_{lj}, \gamma_{ml})$ is a function of the mean parameters of a sample category, gene category, or both.

Claim 6 (Previously Amended) The method according to claim 4 wherein the cellular phenotype is selected from the group comprising, a disease, a cellular process, a physiological pathway, a signaling pathway, a protein expression, or a drug effect.

Claim 7 (Withdrawn) The method according to claim 4 whereby disabilities, medications, comorbidities, laboratory results, and clinical characteristics are linked to a clinical condition in a host.

Claim 8 (Withdrawn) The method according to claim 4 whereby laboratory and observational measurements are linked to physical processes in inorganic substances.

Claim 9 (Withdrawn) The method according to claim 4 whereby chemical substances are linked to their respective pharmacological activities.

Claim 10 (Withdrawn) The method according to claim 4 whereby a financial performance of stocks is identified.

Claim 11 (Currently Amended) A method of determining in a sample a gene or cluster of genes linked to a disease using a microarray, said microarray including at least one known nucleic acid sequence, and expression and position information, comprising:

~~(a)~~ extracting expression and position information from a microarray to generate a set of data corresponding to at least one dimension, said microarray including at least one known nucleic acid sequence, and expression and position information;

~~(b)~~ assigning in a computer to each dimension of the gene or cluster of genes, represented by the microarray, a numerical value;

~~(c)~~ generating in a computer an information algorithm for said extracted information to provide a linking pattern for said gene or cluster of genes; and

~~(d)~~ determining whether the gene or cluster of genes in a sample are linked to the disease by extrapolating from the dimension-based numerical values.

Claim 12 (Original) The method according to claim 11 wherein the information algorithm is constructed in accordance with the formula $\log(Y_{ij}) | i \in S_m, j \in G_l \sim N[t_{il} \cdot f(\alpha_{mt}, \beta_{lj}, \gamma_{ml}), \sigma^2]$, wherein I and j are the expression data by gene and samples respectively; m and l are latent classes on the corresponding dimensions; the t refers to gene expression intensity parameters; and various forms for the function f are chosen~~.~~; and wherein $N[.]$ refers to a Gaussian

distribution; $S_m$ is a latent class m in the first direction; $G_l$ is a latent class 1 in the second direction; and $f(\alpha_{mi}, \beta_{lj}, \gamma_{ml})$ is a function of the mean parameters of a sample category, gene category, or both.

Claim 13 (Currently Amended) A method for identifying in a library a gene or set of genes linked to metastatic properties of a cancer comprising the steps of:

~~(a)~~ providing a nucleic acid material from a suspected cancerous sample;

~~(b)~~ hybridizing the sample-derived process to the library;

~~(c)~~ detecting the differences between hybridization results of the sample and a reference standard;

(d) recording the differences to form a first set of data;

assigning the first set of data to form a first dimension of a matrix in a multidimensional space;

~~(e)~~ analyzing protein expression data to form a second set of data; ~~and~~

assigning the second set of data to form a second dimension of the matrix;

~~(f)~~ combining said first set of data and said second set of data to identify the gene or set of genes which govern metastatic properties of the cancer.

Claim 14 (Currently Amended) The method of claim 13, further comprising:

~~(a)~~ providing a tissue sample from a subject;

~~(b)~~ recording predictive parameters to form a third set of data, wherein the predictive parameters are univariate or multivariate morphometric descriptors; ~~and~~

assigning the third set of data to form a third dimension of the matrix; and

~~(c)~~ combining the first set of data, the second set of data and the third set of data to identify the gene or set of genes which govern metastatic properties of the cancer.

Claim 15 (Previously Amended) The method according to claim 14, wherein the morphometric descriptors are selected from the group comprising optical density, object size, object shape, object color, amount of DNA or RNA, angular second moment, contrast, correlation, difference moment, inverse difference moment, sum average, sum variance, sum entropy, entropy,

difference variance, difference entropy, maximal correlation coefficient, coefficient of variation, peak transition probability, diagonal variance, diagonal moment, second diagonal moment, product moment, triangular symmetry, sum entropy, standard deviation, cell classification (1=Hypodiploid, 2=Diploid, 3=S-Phase, 5=Tetraploid, 6=Hyperploid), blobness, perimeter, DNA index, maximum diameter, minimum diameter, elongation, run length, configurable run length and combination thereof.

Claim 16 (Currently Amended) A method of screening for a drug that modulates an expression of a gene or cluster of genes in a cell of interest comprising the steps of:

~~(a)~~ exposing said cell to said drug;

~~(b)~~ analyzing the gene expression in said cell; and

~~(c)~~ comparing by the method of claim 4 the difference in gene expression of a drug-exposed cell to gene expression of a cell not exposed to the drug or exposed to a drug with known properties.

Claim 17 (Currently Amended) A method for identifying a gene or set of genes linked to a disease of interest comprising the steps of:

~~(a)~~ registering measured observations of the gene or set of genes as variables associated with said disease at a zero time;

~~(b)~~ describing the variables as a matrix in a multidimensional space, wherein each variable represents at least one first and least one second dimension in said space;

~~(c)~~ carrying out, simultaneously or at later times, a series of experimental observations;

~~(d)~~ determining projections of the experimental observations onto the first and second directions, whereby a multivariate model is obtained;

~~(e)~~ updating during the course of the multivariate analysis at least the first and second directions of the matrix in multidimensional space, whereby the multivariate model provides the likelihood of the gene or set of genes being linked to the disease of interest.

Claim 18 (Original) The method of claim 1 wherein said method is used for identifying genes linked to cell or tissue samples collected from a host having or suspected to have a disease comprising the steps of:

(a) assigning in a matrix one or more measurements on each of the genes over a series of experimental or observational conditions;

(b) having genes to form a first direction in a multidimensional space;

(c) allowing cell or tissue samples collected under differing experimental conditions to form a second direction in a multidimensional space;

(d) identifying latent classes of genes in the first direction and latent classes of cell or tissue samples in the principal direction;

(e) calculating the likelihood that each gene is a member of each latent class identified for the first principal direction; and

(f) calculating a likelihood that each cell or tissue sample is a member of each latent class for the second principal direction.

Claim 19 (Canceled)

Claim 20 (Canceled)

Claim 21 (Canceled)

Claim 22 (Canceled)

Claim 23 (Original) A method for analyzing an image of a plurality of objects arranged as an output signal matrix by comparing to a stored output signal matrix database which sets membership rules for the objects of interest, comprising steps:

(a) constructing a stimulated physical matrix comprising an ordered array of objects having X and Y coordinates;

(b) detecting the physical signal at each said object of the physical matrix;

(c) transforming each said physical signal to generate a corresponding electrical output signal;

(d) storing each electrical output signal in an output signal matrix database associating each output signal with the X and Y coordinates of the corresponding physical matrix unit; and

(e) determining the membership of the objects of interest by comparing the output signal matrix database of step (d) with the stored output signal matrix database.

Claim 24 (Previously Added) The method of claim 1 wherein said objects are classified substantially simultaneously.

Claim 25 (New) The method of claim 1 wherein said objects are classified substantially sequentially.